

## SEQUENCE LISTING

## ( 1 ) GENERAL INFORMATION:

( i i ) NUMBER OF SEQUENCES: 12

## ( 2 ) INFORMATION FOR SEQ ID NO: 1:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 275 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Aspergillus giganteus*

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 5'UTR
- ( B ) LOCATION: 1..45

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 46..225
- ( C ) IDENTIFICATION METHOD: experimental
- ( D ) OTHER INFORMATION: /codon\_start= 46
  - / function= "antifungal agent"
  - / product= "antifungal peptide"
  - / evidence= EXPERIMENTAL
  - / note= "antifungal agent, especially on *Rhizoctonia solani*, various *Aspergillus*, *Fusaria* and *Trichophyton* species"

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

TTGCCACCCC CGTTGAAGCC GATTCTCTCA CCGCTGGTGG TCTGG ATG CAA GAG      54
                               Met Gln Glu
                               1
ATG AGA GCG CGG GTT TTG GCC ACA TAC AAT GGC AAA TGC TAC AAG AAG      102
Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys
      5              10              15
GAT AAT ATC TGC AAG TAC AAG GCA CAG AGC GGC AAG ACT GCC ATT TGC      150
Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys
      20              25              30              35
AAG TGC TAT GTC AAA AAG TGC CCC CGC GAC GGC GCG AAA TGC GAG TTT      198
Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe
              40              45              50
GAC AGC TAC AAG GGG AAG TGC TAC TGC TAGACGGTGA GCGAAGGGAC      245
Asp Ser Tyr Lys Gly Lys Cys Tyr Cys
      55              60
GAAGTAGGCT GGGGGTTATT TTACTCTGCT      275

```

## ( 2 ) INFORMATION FOR SEQ ID NO: 2:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 60 amino acids
- ( B ) TYPE: amino acid
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Gln Glu Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys
 1              5              10              15
Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr
      20              25              30

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Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys  
           35                  40                  45  
 Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys  
       50                  55                  60

## ( 2 ) INFORMATION FOR SEQ ID NO: 3:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 51 amino acids
- ( B ) TYPE: amino acid
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: protein

## ( v ) FRAGMENT TYPE: C-terminal

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Aspergillus giganteus*

## ( i x ) FEATURE:

- ( A ) NAME/KEY: Protein
- ( B ) LOCATION: 1..51
- ( D ) OTHER INFORMATION: /note= "active protein fragment of AFP"

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp Asn Ile Cys Lys Tyr  
 1                  5                  10                  15  
 Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys Cys Tyr Val Lys Lys  
           20                  25                  30  
 Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys  
           35                  40                  45  
 Cys Tyr Cys  
       50

## ( 2 ) INFORMATION FOR SEQ ID NO: 4:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 1032 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Hordeum vulgare*
- ( B ) STRAIN: Lev. Piggy

## ( v i i ) IMMEDIATE SOURCE:

- ( A ) LIBRARY: cDNA gene bank in lambda-gt-11-phages

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 5'UTR
- ( B ) LOCATION: 1..42

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 43..885
- ( D ) OTHER INFORMATION: /codon\_start= 43  
                   / function= "antifungal activity"  
                   / product= "protein synthesis inhibitor (PSI)"  
                   / note= "antifungal activity, especially on spores  
                   of *Trichoderma reesei* and *Fusarium sporotrichoides*  
                   and on *Rhizoctonia solani*."

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 3'UTR
- ( B ) LOCATION: 886..1032
- ( D ) OTHER INFORMATION: /partial  
                   / note= "46 nucleotides at the 3'-end not shown."

## ( i x ) FEATURE:

CTTAATAGCA CATCTTGTCG GTCTTAGCTT TGCATTACAT CC ATG GCG GCA AAG																54
Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr ACC GCG ACG TTC AAC GTC																
5 10 15 20																
CAG	GCC	AGC	TCC	GCC	GAC	TAC	GCC	ACC	TTC	ATC	GCC	GGC	ATC	CGC	AAC	150
Gln	Ala	Ser	Ser	Ala	Asp	Tyr	Ala	Thr	Phe	Ile	Ala	Gly	Ile	Arg	Asn	
25 30 35																
AAG	CTC	CGC	AAC	CCG	GCG	CAC	TTC	TCC	CAC	AAC	CGC	CCC	GTG	CTG	CCG	198
Lys	Leu	Arg	Asn	Pro	Ala	His	Phe	Ser	His	Asn	Arg	Pro	Val	Leu	Pro	
40 45 50																
CCG	GTC	GAG	CCC	AAC	GTC	CCG	CCG	AGC	AGG	TGG	TTC	CAC	GTC	GTG	CTC	246
Pro	Val	Glu	Pro	Asn	Val	Pro	Pro	Ser	Arg	Trp	Phe	His	Val	Val	Leu	
55 60 65																
AAG	GCC	TCG	CCG	ACC	AGC	GCC	GGG	CTC	ACG	CTG	GCC	ATT	CGG	GCG	GAC	294
Lys	Ala	Ser	Pro	Thr	Ser	Ala	Gly	Leu	Thr	Leu	Ala	Ile	Arg	Ala	Asp	
70 75 80																
AAC	ATC	TAC	CTG	GAG	GGC	TTC	AAG	AGC	AGC	GAC	GGC	ACC	TGG	TGG	GAG	342
Asn	Ile	Tyr	Leu	Glu	Gly	Phe	Lys	Ser	Ser	Asp	Gly	Thr	Trp	Trp	Glu	
85 90 95 100																
CTC	ACC	CCG	GGC	CTC	ATC	CCC	GGC	GGC	ACC	TAC	GTC	GGG	TTC	GGC	GGC	390
Leu	Thr	Pro	Gly	Leu	Ile	Pro	Gly	Gly	Thr	Tyr	Val	Gly	Phe	Gly	Gly	
105 110 115																
ACC	TAC	CGC	GAC	CTC	CTC	GGC	GAC	ACC	GAC	AAG	CTG	ACC	AAC	GTC	GCT	438
Thr	Tyr	Arg	Asp	Leu	Leu	Gly	Asp	Thr	Asp	Lys	Leu	Thr	Asn	Val	Ala	
120 125 130																
CTC	GGC	CGG	CAG	CAG	CTC	CCG	GAC	GCG	GTG	ACC	GCC	CTC	CAC	GGG	CGC	486
Leu	Gly	Arg	Gly	Gln	Leu	Pro	Asp	Ala	Val	Thr	Ala	Leu	His	Gly	Arg	
135 140 145																
ACC	AAG	GCC	GAC	AAG	CCG	TCC	GGC	CCG	AAG	CAG	CAG	CAG	GCG	AGG	GAG	534
Thr	Lys	Ala	Asp	Lys	Pro	Ser	Gly	Pro	Lys	Gln	Gln	Gln	Ala	Arg	Glu	
150 155 160																
GCG	GTG	ACG	ACG	CTG	CTC	CTC	ATG	GTG	AAC	GAG	GCC	ACG	CGG	TTC	CAG	582
Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala	Thr	Arg	Phe	Gln	
165 170 175																
ACG	GTG	TCT	GGG	TTC	GTG	GCC	GGG	TTG	CTG	CAC	CCC	AAG	GCG	GTG	GAG	630
Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro	Lys	Ala	Val	Glu	
185 190 195																
AAG	AAG	AGC	GGG	AAG	ATC	GGC	AAT	GAG	ATG	AAG	GCC	CAG	GTG	AAC	GGG	678
Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Glu	Met	Lys	Ala	Gln	Val	Asn	Gly	
200 205 210																

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TGG	CAG	GAC	CTG	TCC	GCG	GCG	CTG	CTG	AAG	ACG	GAC	GTG	AAG	CCT	CCG	726
Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	Val	Lys	Pro	Pro	
		215					220					225				
CCG	GGA	AAG	TCG	CCA	GCG	AAG	TTC	GCG	CCG	ATC	GAG	AAG	ATG	GGC	GTG	774
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Ala	Pro	Ile	Glu	Lys	Met	Gly	Val	
	230					235					240					
AGG	ACG	GCT	GTA	CAG	GCC	GCC	AAC	ACG	CTG	GGG	ATC	CTG	CTG	TTC	GTG	822
Arg	Thr	Ala	Val	Gln	Ala	Ala	Asn	Thr	Leu	Gly	Ile	Leu	Leu	Phe	Val	
245					250					255					260	
GAG	GTG	CCG	GGT	GGG	TTG	ACG	GTG	GCC	AAG	GCG	CTG	GAG	CTG	TTC	CAT	870
Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu	Glu	Leu	Phe	His	
				265					270					275		
GCG	AGT	GGT	GGG	AAA	TAGGTAGTTT	TCCAGGTATA	CCTGCATGGG	TAGTGTAATA								925
Ala	Ser	Gly	Gly	Lys												
			280													
GTCGAATAAA	CATGTCACAG	AGTGACGGAC	TGATATAAAT	AAATAAATAA	ACGTGTCACA											985
GAGTTACATA	TAAACAAATA	AATAAATAAT	TAAAAATGTC	CAGTTTA												1032

( 2 ) INFORMATION FOR SEQ ID NO: 5:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 281 amino acids

( B ) TYPE: amino acid

( D ) TOPOLOGY: linear

( ii ) MOLECULE TYPE: protein

( xi ) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Ala	Ala	Lys	Met	Ala	Lys	Asn	Val	Asp	Lys	Pro	Leu	Phe	Thr	Ala	
1				5					10					15		
Thr	Phe	Asn	Val	Gln	Ala	Ser	Ser	Ala	Asp	Tyr	Ala	Thr	Phe	Ile	Ala	
		20						25					30			
Gly	Ile	Arg	Asn	Lys	Leu	Arg	Asn	Pro	Ala	His	Phe	Ser	His	Asn	Arg	
		35					40					45				
Pro	Val	Leu	Pro	Pro	Val	Glu	Pro	Asn	Val	Pro	Pro	Ser	Arg	Trp	Phe	
	50					55					60					
His	Val	Val	Leu	Lys	Ala	Ser	Pro	Thr	Ser	Ala	Gly	Leu	Thr	Leu	Ala	
65				70						75					80	
Ile	Arg	Ala	Asp	Asn	Ile	Tyr	Leu	Glu	Gly	Phe	Lys	Ser	Ser	Asp	Gly	
			85					90						95		
Thr	Trp	Trp	Glu	Leu	Thr	Pro	Gly	Leu	Ile	Pro	Gly	<u>Gly</u>	Thr	Tyr	Val	
			100					105				<u>Ala</u>	110			
Gly	Phe	Gly	Gly	Thr	Tyr	Arg	Asp	Leu	Leu	Gly	Asp	Thr	Asp	Lys	Leu	
		115					120					125				
Thr	Asn	Val	Ala	Leu	Gly	Arg	Gln	Gln	Leu	<u>Pro</u>	Asp	Ala	Val	Thr	Ala	
	130					135				<u>Ala</u>	140					
Leu	His	Gly	Arg	Thr	Lys	Ala	Asp	Lys	Pro	Ser	Gly	Pro	Lys	Gln	Gln	
145					150					155				160		
Gln	Ala	Arg	Gln	Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala	
			165					170						175		
Thr	Arg	Phe	Gln	Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro	
		180					185					190				
Lys	Ala	Val	Glu	Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Gln	Met	Lys	Ala	
	195						200					205				
Gln	Val	Asn	Gly	Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	
	210					215					220					
Val	Lys	Pro	Pro	Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Ala	Pro	Ile	Glu	
225					230					235					240	

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Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile  
 245 250 255  
 Leu Leu Phe Val Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu  
 260 265 270  
 Glu Leu Phe His Ala Ser Gly Gly Lys

( 2 ) INFORMATION FOR SEQ ID NO: 6:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 480 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Hordeum vulgare
- ( B ) STRAIN: Lcv. Piggy

## ( v i i ) IMMEDIATE SOURCE:

- ( A ) LIBRARY: cDNA gene bank in lambda-gt-11-phages
- ( B ) CLONE: incomplete psi cDNA clone

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 1..351
- ( D ) OTHER INFORMATION: /partial  
 / codon\_start= 1  
 / function= "protein synthesis inhibitor"  
 / product= "protein synthesis inhibitor"  
 / standard\_name= "PSI"  
 / note= "aminoterminally incomplete protein from  
 an incomplete PSI cDNA clone"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 3'UTR
- ( B ) LOCATION: 352..487

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 404..409
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
 signal"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 437..442
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
 signal"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 445..450
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
 signal"

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCG GTG ACG ACG CTG CTC CTC ATG GTG AAC GAG GCC ACG CGG TTC CAG	48
Ala Val Thr Thr Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln	
1 5 10 15	
ACG GTG TCG GGG TTC GTG GCC GGG CTG CTG CAC CCC AAG GCG GTG GAG	96
Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu	
20 25 30	
AAG AAG AGC GGG AAG ATC GGC AAT GAG ATG AAG GCC CAG GTG AAC GGG	144
Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly	
35 40 45	
TGG CAG GAC CTG TCC GCG GCG CTG CTG AAG ACG GAC GTG AAG CCC CCG	192
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro	
50 55 60	

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CCG	GGA	AAG	TCG	CCA	GCG	AAG	TTC	ACG	CCG	ATC	GAG	AAG	ATG	GGC	GTG	240
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Thr	Pro	Ile	Glu	Lys	Met	Gly	Val	
65					70				75					80		
AGG	ACT	GCT	GAG	CAG	GCT	GCG	GCT	ACT	TTG	GGG	ATC	CTG	CTG	TTC	GTT	288
Arg	Thr	Ala	Glu	Gln	Ala	Ala	Ala	Thr	Leu	Gly	Ile	Leu	Leu	Phe	Val	
			85						90					95		
GAG	GTG	CCG	GGT	GGG	TTG	ACG	GTG	GCC	AAG	GCG	CTG	GAG	CTG	TTT	CAT	336
Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu	Glu	Leu	Phe	His	
			100					105					110			
GCG	AGT	GGT	GGG	AAA	TAGGTAGTTT	TGCAGGTATA	CCTGCATGGG	TAAATGTAAA								391
Ala	Ser	Gly	Gly	Lys												
			115													
AGTCGAATAA	AAATGTCACA	GAGTGACGGA	CTGATATAAA	TAAATTAATA	AACATGTCAT											451
CATGAGTGAC	AGACTGATAT	AAATAAATA														480

( 2 ) INFORMATION FOR SEQ ID NO: 7:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 117 amino acids  
 ( B ) TYPE: amino acid  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala	Thr	Arg	Phe	Gln	
1				5					10					15		
Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro	Lys	Ala	Val	Glu	
			20					25					30			
Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Glu	Met	Lys	Ala	Gln	Val	Asn	Gly	
		35					40					45				
Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	Val	Lys	Pro	Pro	
	50					55					60					
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Thr	Pro	Ile	Glu	Lys	Met	Gly	Val	
	65				70					75					80	
Arg	Thr	Ala	Glu	Gln	Ala	Ala	Ala	Thr	Leu	Gly	Ile	Leu	Leu	Phe	Val	
			85						90					95		
Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu	Glu	Leu	Phe	His	
			100					105					110			
Ala	Ser	Gly	Gly	Lys												
			115													

( 2 ) INFORMATION FOR SEQ ID NO: 8:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 2329 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: single  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Serratia marcescens*

( v i i ) IMMEDIATE SOURCE:

( A ) LIBRARY: Cosmid bank from *Serratia marcescens*

( i x ) FEATURE:

- ( A ) NAME/KEY: misc\_feature  
 ( B ) LOCATION: 1..2329  
 ( C ) IDENTIFICATION METHOD: experimental  
 ( D ) OTHER INFORMATION: /function="exo-chitinase"  
 / product= "ChS protein"  
 / evidence= EXPERIMENTAL

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/ note= "sequence listing of the ChiS gene from a  
plasmid pLChiS from E.coli A 5187"

( \* i ) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CAGGGCGTTG	TCAATAATGA	CAACACCCTG	GCTGAAGAGT	GTGGTGCAAT	ACTGATAAAT	60
ATTTATCTTT	CCTTAATAGA	AAATTCAC TA	TCCTTATTTG	TCATGTTTTT	TTTTATTTAT	120
ATGAAAATAA	ATTACAGCTT	GCTGAATAAA	ACCCAGTTGA	TAGCGCTCTT	GTTTTTGCGC	180
CTTTTTTATT	TATAGTACTG	AATGTACGCG	GTGGGAATGA	TTATTTTCGCC	ACGTGGAAG	240
ACGCTGTTGT	TATTTATTGA	TTTAAACCTT	CGCGGATTAT	TGCGGAATTT	TTTCGCTTCG	300
GCAATGCATC	GCGACGATTA	ACTCTTTTAT	GTTTATCCTC	TCGGAATAAA	GGAATCAGTT	360
ATGCGCAAAAT	TTAATAAAC	GCTGTTGGCG	CTGTTGATCG	GCAGCACGCT	GTGTTCCGCG	420
GCGCAGGCCG	CCGCGCCGGG	CAAGCCGACC	ATCGCCTGGG	GCAACACCAA	GTTCCGCCATC	480
GTTGAAGTTG	ACCAGGCGGC	TACCGCTTAT	AATAATTTGG	TGAAAGGTAA	AAATGCCGCC	540
GATGTTTCCG	TCTCCTGGAA	TTTATGGAAT	GGCGACACCG	GCACGACGGC	AAAAGTTTTA	600
TTAAATGGCA	AAGAGGCGTG	GAGTGGTCCT	TCAACCGGAT	CTTCCGGTAC	GGCGAATTTT	660
AAAGTGAATA	AAGGCGGCCG	TTATCAAATG	CAGGTGGCAC	TGTGCAATGC	CGACGGCTGC	720
ACCGCCAGTG	ACGCCACCGA	AATTGTGGTA	GCCGACACCG	ACGGCAGCCA	TTTGGCGCCG	780
TTGAAAGAGC	CGCTGCTGGA	AAAGAATAAA	CCGTATAAAC	AGAACTCCGG	CAAAGTGGTC	840
GGTTCTTATT	TCGTCGAGTG	GGGCGTTTAC	GGGCGCAATT	TCACCGTCGA	CAAGATCCCG	900
GCGCAAAACC	TGACCCACCT	GCTGTACGGC	TTTATCCCGA	TCTGCGGCGG	CAATGGCATC	960
AACGACAGCC	TGAAAGAGAT	TGAAGGCAGC	TTCCAGGCGT	TGCAGCGCTC	CTGCCAGGGC	1020
CGCGAGGACT	TCAAAGTCTC	GATCCACGAT	CCGTTTCGCC	CGCTGCAAAA	AGCGCAGAAG	1080
GGCGTGACCG	CCTGGGATGA	CCCCTACAAG	GGCAACTTCG	GCCAGCTGAT	GGCGCTGAAG	1140
CAGGCGCATC	CTGACCTGAA	AATCCTGCCG	TCGATCGGCG	GCTGGACGCT	GTCCGACCCG	1200
TTCTTCTTCA	TGGGCGACAA	GGTGAAGCGC	GATCGCTTCG	TCGGTTCGGT	GAAAGAGTTC	1260
CTGCAGACCT	GGAAGTTCTT	CGACGGCGTG	GATATCGACT	GGGAGTTCCC	GGGCGGCAAA	1320
GGCGCCAACC	CTAACCTGGG	CAGCCCGCAA	GACGGGGAAA	CCTATGTGCT	GCTGATGAAG	1380
GAGCTGCGGG	CGATGCTGGA	TCAGCTGTCT	GTGGAAACCG	GCCGCAAGTA	TGAGCTGACC	1440
TCCGCCATCA	GCGCCGGTAA	GGACAAGATC	GACAAGGTGG	CTTACAACGT	TGCGCAGAAC	1500
TCGATGGATC	ACATCTTCCT	GATGAGCTAC	GACTTCTATG	GCGCCTTCGA	TCTGAAGAAC	1560
CTGGGGCATC	AGACCGCGCT	GAATGCGCCG	GCCTGGAAC	CGGACACCGC	CTACACCACG	1620
GTGAACGGCG	TCAATGCGCT	GCTGGCGCAG	GGCGTCAAGC	CGGGCAAAAT	CGTCGTCCGC	1680
ACCGCCATGT	ATGGCCGCGG	CTGGACCGGG	GTGAACGGCT	ACCAGAACAA	TATTCGGTTC	1740
ACCGGCACCG	CCACCGGGCC	GGTTAAAGGC	ACCTGGGAGA	ACGGTATCGT	GGACTACCGC	1800
CAAATCGCCG	GCCAGTTCAT	GAGCGGCGAG	TGGCAGTATA	CCTACGACGC	CACGGCGGAA	1860
GCGCCTTACG	TGTTCAAACC	TTCCACCGGC	GATCTGATCA	CTTCGACGA	TGCCCGCTCG	1920
GTGCAGGCTA	AAGGCAAGTA	CGTGTTGGAT	AAGCAGCTGG	GCGGCCTGTT	CTCCTGGGAG	1980
ATCGACGCGG	ATAACGGCGA	TATTCTCAAC	AGCATGAACG	CCAGCCTGGG	CAACAGCGCC	2040
GGCGTTCAAT	AATCGGTTGC	AGTGGTTGCC	GGGGGATATC	CTTTCGCCCC	CGGCTTTTTT	2100
GCCGACGAAA	GTTTTTTTAC	GCCGCACAGA	TTGTGGCTCT	GCCCCGAGCA	AAACGCGCTC	2160
ATCGGACTCA	CCCTTTTGGG	TAATCCTTCA	GCATTTCTCT	CTGTCTTTAA	CGGCGATCAC	2220
AAAAATAACC	GTTTCAGATAT	TCATCATTCA	GCAACAAAGT	TTTGGCGTTT	TTTAACGGAG	2280

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TTAAAAACCA GTAAGTTTGT GAGGGTCAGA CCAATGCGCT AAAAAATGGG

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## ( 2 ) INFORMATION FOR SEQ ID NO: 9:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 1002 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Hordeum vulgare*
- ( B ) STRAIN: L

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 5'UTR
- ( B ) LOCATION: 1..63

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 64..861
- ( D ) OTHER INFORMATION: /codon\_start= 64  
/ function= "chitinase"  
/ product= "26 kD preprotein of chitinase G (ChiG)"  
/ note= "antifungal activity, especially on  
*Trichoderma reesei* and *Fusarium sporotrichoides* as  
well as *Rhizoctonia solani* and *Botrytis cinerea*."

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 3'UTR
- ( B ) LOCATION: 862..1002
- ( D ) OTHER INFORMATION: /partial  
/ note= "11 nucleotides at 3' end not shown"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 905..910
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 64..294
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 298..312
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 349..378
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 466..588
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 607..861
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: mat\_peptide
- ( B ) LOCATION: 133..861

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 9:



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CCTACGACAG	TAGCGTAACG	GTAACACCG	AGTACGGTAC	TCTGTGCTTT	GTTGGCTCGC	60										
ACA Met -23	ATG Arg	AGA Ser	TCG Ser	CTC Leu -20	GCG Ala	GTG Val	GTG Val	GTG Val	GCC Ala -15	GTG Val	GTA Val	GCC Ala	ACG Thr	GTG Val -10	GCC Ala	108
ATG Met	GCC Ala	ATC Ile	GGC Gly -5	ACG Thr	GCG Ala	CGC Arg	GGC Gly	AGC Ser 1	GTG Val	TCC Ser	TCC Ser	ATC Ile 5	GTC Val	TCG Ser	CGC Arg	156
GCA Ala	CAG Gln	TTT Phe	GAC Asp	CGC Arg	ATG Met	CTT Leu 15	CTC Leu	CAC His	CGC Arg	AAC Asn	GAC Asp 20	GGC Gly	GCC Ala	TGC Cys	CAG Gln	204
GCC Ala 25	AAG Lys	GGC Gly	TTC Phe	TAC Tyr	ACC Thr 30	TAC Tyr	GAC Asp	GCC Ala	TTC Phe	GTC Val 35	GCC Ala	GCC Ala	GCA Ala	GCC Ala	GCC Ala 40	252
TTC Phe	CCG Pro	GGC Gly	TTC Phe	GGC Gly 45	ACC Thr	ACC Thr	GGC Gly	AGC Ser	GCC Ala 50	GAC Asp	GCC Ala	CAG Gln	AAG Lys	CGC Arg 55	GAG Glu	300
GTG Val	GCC Ala	GCC Ala	TTC Phe 60	CTA Leu	GCA Ala	CAG Gln	ACC Thr	TCC Ser 65	CAC His	GAG Glu	ACC Thr	ACC Thr	GGC Gly 70	GGG Gly	TGG Trp	348
GCG Ala	ACT Thr	GCA Ala 75	CCG Pro	GAC Asp	GGG Gly	GCC Ala	TTC Phe 80	GCC Ala	TGG Trp	GGC Gly	TAC Tyr	TGC Cys 85	TTC Phe	AAG Lys	CAG Gln	396
GAA Glu	CGT Arg 90	GGC Gly	GCC Ala	TCC Ser	TCC Ser	GAC Asp 95	TAC Tyr	TGC Cys	ACC Thr	CCG Pro	AGC Ser 100	GCA Ala	CAA Gln	TGG Trp	CCG Pro	444
TGC Cys 105	GCC Ala	CCC Pro	GGG Gly	AAG Lys 110	CGC Arg	TAC Tyr	TAC Tyr	GGC Gly	CGC Arg	GGG Gly 115	CCA Pro	ATC Ile	CAG Gln	CTC Leu	TCC Ser 120	492
CAC His	AAC Asn	TAC Tyr	AAC Asn	TAT Tyr 125	GGA Gly	CCT Pro	GCC Ala	GGC Gly	CGG Arg 130	GCC Ala	ATC Ile	GGG Gly	GTC Val	GAT Asp 135	CTG Leu	540
CTG Leu	GCC Ala	AAC Asn	CCG Pro 140	GAC Asp	CTG Leu	GTG Val	GCC Ala	ACG Thr 145	GAC Asp	GCC Ala	ACT Thr	GTG Val	GGC Gly 150	TTT Phe	AAG Lys	588
ACG Thr	GCC Ala	ATC Ile 155	TGG Trp	TTC Phe	TGG Trp	ATG Met	ACG Thr 160	GCG Ala	CAG Gln	CCG Pro	CCC Pro	AAG Lys 165	CCA Pro	TCG Ser	AGC Ser	636
CAT His	GCT Ala	GTG Val	ATC Ile	GCC Ala	GGC Gly	CAG Gln	TGG Trp 175	AGC Ser	CCG Pro	TCA Ser	GGG Gly 180	GCT Ala	GAC Asp	CGG Arg	GCC Ala	684
GCA Ala 185	GGC Gly	CGG Arg	GTG Val	CCC Pro	GGG Gly	TTT Phe	GGT Gly	GTG Val	ATC Ile	ACC Thr 195	AAC Asn	ATC Ile	ATC Ile	AAC Asn	GGC Gly 200	732
GGG Gly	ATC Ile	GAG Glu	TGC Cys	GGT Gly 205	CAC His	GGG Gly	CAG Gln	GAC Asp	AGC Ser 210	CGC Arg	GTC Val	GCC Ala	GAT Asp	CGA Arg 215	ATC Ile	780
GGG Gly	TTT Phe	TAC Tyr	AAG Lys 220	CGC Arg	TAC Tyr	TGT Cys	GAC Asp	ATC Ile 225	CTC Leu	GGC Gly	GTT Val	GGC Gly	TAC Tyr 230	GGC Gly	AAC Asn	828
AAC Asn	CTC Leu	GAT Asp 235	TGC Cys	TAC Tyr	AGC Ser	CAG Gln	AGA Arg 240	CCC Pro	TTC Phe	GCC Ala	TAATTAATTA	GTCATGTATT				881
AATCTTGGCC	CTCCATAAAA	TACAATAAGA	GCATCGTCTC	CTATCTACAT	GCTGTAAGAT											941
GTAACCTATGG	TAACCTTTTA	TGGGGAACAT	AACAAAGGCA	TCTCGTATAG	ATGCTTTTGT											1001
A																1002

( 2 ) INFORMATION FOR SEQ ID NO:10:

( i ) SEQUENCE CHARACTERISTICS:

-continued

( A ) LENGTH: 266 amino acids  
( B ) TYPE: amino acid  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met -23	Arg	Ser	Leu -20	Ala	Val	Val	Val	Ala -15	Val	Val	Ala	Thr	Val -10	Ala	Met
Ala	Ile	Gly -5	Thr	Ala	Arg	Gly	Ser 1	Val	Ser	Ser	Ile 5	Val	Ser	Arg	Ala
Gln 10	Phe	Asp	Arg	Met	Leu 15	Leu	His	Arg	Asn	Asp 20	Gly	Ala	Cys	Gln	Ala 25
Lys	Gly	Phe	Tyr	Thr 30	Tyr	Asp	Ala	Phe	Val 35	Ala	Ala	Ala	Ala	Ala 40	Phe
Pro	Gly	Phe	Gly 45	Thr	Thr	Gly	Ser	Ala 50	Asp	Ala	Gln	Lys	Arg 55	Glu	Val
Ala	Ala	Phe 60	Leu	Ala	Gln	Thr	Ser 65	His	Glu	Thr	Thr	Gly 70	Gly	Trp	Ala
Thr	Ala 75	Pro	Asp	Gly	Ala	Phe 80	Ala	Trp	Gly	Tyr	Cys 85	Phe	Lys	Gln	Glu
Arg 90	Gly	Ala	Ser	Ser	Asp 95	Tyr	Cys	Thr	Pro	Ser 100	Ala	Gln	Trp	Pro	Cys 105
Ala	Pro	Gly	Lys	Arg 110	Tyr	Tyr	Gly	Arg	Gly 115	Pro	Ile	Gln	Leu	Ser 120	His
Asn	Tyr	Asn	Tyr 125	Gly	Pro	Ala	Gly	Arg 130	Ala	Ile	Gly	Val	Asp 135	Leu	Leu
Ala	Asn	Pro 140	Asp	Leu	Val	Ala	Thr 145	Asp	Ala	Thr	Val	Gly 150	Phe	Lys	Thr
Ala	Ile 155	Trp	Phe	Trp	Met	Thr 160	Ala	Gln	Pro	Pro	Lys 165	Pro	Ser	Ser	His
Ala 170	Val	Ile	Ala	Gly	Gln 175	Trp	Ser	Pro	Ser	Gly 180	Ala	Asp	Arg	Ala	Ala 185
Gly	Arg	Val	Pro	Gly 190	Phe	Gly	Val	Ile	Thr 195	Asn	Ile	Ile	Asn	Gly 200	Gly
Ile	Glu	Cys	Gly 205	His	Gly	Gln	Asp	Ser 210	Arg	Val	Ala	Asp	Arg 215	Ile	Gly
Phe	Tyr	Lys 220	Arg	Tyr	Cys	Asp	Ile 225	Leu	Gly	Val	Gly	Tyr 230	Gly	Asn	Asn
Leu	Asp 235	Cys	Tyr	Ser	Gln	Arg 240	Pro	Phe	Ala						

( 2 ) INFORMATION FOR SEQ ID NO:11:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 1235 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Hordeum vulgare*  
( B ) STRAIN: L

( i x ) FEATURE:

( A ) NAME/KEY: 5'UTR  
( B ) LOCATION: 1..48

( i x ) FEATURE:

( A ) NAME/KEY: CDS

-continued

( B ) LOCATION: 49..1050  
 ( D ) OTHER INFORMATION: /partial  
     / codon\_start= 49  
     / function= "glucanase"  
     / product= "preprotein of the glucanase GluG"

( i x ) FEATURE:  
     ( A ) NAME/KEY: 3'UTR  
     ( B ) LOCATION: 1051..1235  
     ( D ) OTHER INFORMATION: /partial  
         / note= "14 nucleotides at the 3'end not shown."

( i x ) FEATURE:  
     ( A ) NAME/KEY: polyA\_signal  
     ( B ) LOCATION: 1083..1088  
     ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
         signal"

( i x ) FEATURE:  
     ( A ) NAME/KEY: polyA\_signal  
     ( B ) LOCATION: 1210..1215  
     ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
         signal"

( i x ) FEATURE:  
     ( A ) NAME/KEY: mat\_peptide  
     ( B ) LOCATION: 133..1050

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCAGCATTG CATAGCATTT GAGCACCAGA TACTCCGTGT GTGCACCA ATG GCT AGA	57
Met Ala Arg	
- 28	
AAA GAT GTT GCC TCC ATG TTT GCA GTT GCT CTC TTC ATT GGA GCA TTC	105
Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe	
- 25 - 20 - 15 - 10	
GCT GCT GTT CCT ACG AGT GTG CAG TCC ATC GGC GTA TGC TAC GGC GTG	153
Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val	
- 5 1 5	
ATC GGC AAC AAC CTC CCC TCC CGG AGC GAC GTG GTG CAG CTC TAC AGG	201
Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg	
10 15 20	
TCC AAG GGC ATC AAC GGC ATG CGC ATC TAC TTC GCC GAC GGG CAG GCC	249
Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala	
25 30 35	
CTC TCG GCC GTC CGC AAC TCC GGC ATC GGC CTC ATC CTC GAC ATC GGC	297
Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu Asp Ile Gly	
40 45 50 55	
AAC GAC CAG CTC GCC AAC ATC GCC GCC AGC ACC TCC AAC GCG GCC TCC	345
Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn Ala Ala Ser	
60 65 70	
TGG GTC CAG AAC AAC GTG CGG CCC TAC TAC CCT GCC GTG AAC ATC AAG	393
Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val Asn Ile Lys	
75 80 85	
TAC ATC GCC GCC GGC AAC GAG GTG CAG GGC GGC GCC ACG CAG AGC ATC	441
Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr Gln Ser Ile	
90 95 100	
CTG CCG GCC ATG CGC AAC CTC AAC GCG GCC CTC TCC GCG GCG GGG CTC	489
Leu Pro Ala Met Arg Asn Ala Asn Ala Ala Leu Ser Ala Ala Gly Leu	
105 110 115	
GGC GCC ATC AAG GTG TCC ACC TCC ATC CGG TTC GAC GAG GTG GCC AAC	537
Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu Val Ala Asn	
120 125 130 135	
TCC TTC CCG CCC TCC GCC GGC GTG TTC AAG AAC GCC TAC ATG ACG GAC	585
Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr Met Thr Asp	
140 145 150	

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-continued

GTG Val	GCC Ala	CGG Arg	CTC Leu 155	CTG Leu	GCG Ala	AGC Ser	ACC Thr	GGC Gly 160	GCG Ala	CCG Pro	CTG Leu	CTC Leu	GCC Ala 165	AAC Asn	GTC Val	633		
TAC Tyr	CCC Pro	TAC Tyr 170	TTC Phe	GCG Ala	TAC Tyr	CGT Arg	GAC Asp 175	AAC Asn	CCC Pro	GGG Gly	AGC Ser	ATC Ile 180	AGC Ser	CTG Leu	AAC Asn	681		
TAC Tyr	GCG Ala 185	ACG Thr	TTC Phe	CAG Gln	CCG Pro	GGC Gly 190	ACC Thr	ACC Thr	GTG Val	CGT Arg	GAC Asp 195	CAG Gln	AAC Asn	AAC Asn	GGG Gly	729		
CTG Leu 200	ACC Thr	TAC Tyr	ACG Thr	TCC Ser	CTG Leu 205	TTC Phe	GAC Asp	GCG Ala	ATG Met	GTG Val 210	GAC Asp	GCC Ala	GTG Val	TAC Tyr	GCG Ala 215	777		
GCG Ala	CTG Leu	GAG Glu	AAG Lys	GCC Ala 220	GGC Gly	GCG Ala	CCG Pro	GCG Ala	GTG Val 225	AAG Lys	GTG Val	GTG Val	GTG Val	TCG Ser 230	GAG Glu	825		
AGC Ser	GGG Gly	TGG Trp	CCG Pro 235	TCG Ser	GCG Ala	GGC Gly	GGG Gly 240	TTT Phe	GCG Ala	GCG Ala	TCG Ser	GCC Ala	GGC Gly 245	AAT Asn	GCG Ala	873		
CGG Arg	ACG Thr	TAC Tyr 250	AAC Asn	CAG Gln	GGG Gly	CTG Leu	ATC Ile 255	AAC Asn	CAC His	GTC Val	GGC Gly	GGG Gly 260	GGC Gly	ACG Thr	CCC Pro	921		
AAG Lys	AAG Lys 265	CGG Arg	GAG Gln	GCG Ala	CTG Leu	GAG Glu 270	ACG Thr	TAC Tyr	ATC Ile	TTC Phe	GCC Ala 275	ATG Met	TTC Phe	AAC Asn	GAG Glu	969		
AAC Asn 280	CAG Gln	AAG Lys	ACC Thr	GGG Gly	GAC Asp 285	GCC Ala	ACG Thr	GAG Glu	AGG Arg	AGC Ser 290	TTC Phe	GGG Gly	CTC Leu	TTC Phe	AAC Asn 295	1017		
CCG Pro	GAC Asp	AAG Lys	TCG Ser	CCG Pro 300	GCA Ala	TAC Tyr	AAC Asn	ATC Ile	CAG Gln 305	TTC Phe	TAGTACGTGT				AGCTACCTAG		1070	
CTCACATAACC			TAAATAAATA			AGCTGCACGT			ACGTACGTAA			TGCGGCATCC			AAGTGTAACG			1130
TAGACACGTA			CATTTCATCCA			TGGAAGAGTG			CAACCAAGCA			TGCGTTAACT			TCCTGGTGAT			1190
GATACATCAT			CATGGTATGA			ATAAAAAGATA			TGGAAGATGT			TATGA						1235

## ( 2 ) INFORMATION FOR SEQ ID NO: 12:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 334 amino acids  
 ( B ) TYPE: amino acid  
 ( D ) TOPOLOGY: linear

## ( ii ) MOLECULE TYPE: protein

## ( xi ) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

Met Ala Arg Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile
-28          -25          -20          -15

Gly Ala Phe Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys
-10          -5          1

Tyr Gly Val Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln
5          10          15          20

Leu Tyr Arg Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp
25          30          35

Gly Gln Ala Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu
40          45          50

Asp Ile Gly Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn
55          60          65

Ala Ala Ser Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val
70          75          80

```

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Logemann, Juergen
- (B) STREET: Lavendeltuyn 5
- (C) CITY: NB Leiden
- (E) COUNTRY: The Netherlands
- (F) POSTAL CODE (ZIP): 2317
  
- (A) NAME: Jach, Guido
- (B) STREET: Maternusstrasse 22
- (C) CITY: Koeln
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 50678
  
- (A) NAME: Goernhardt, Birgit
- (B) STREET: Auf dem Knoepp 28
- (C) CITY: Koeln
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 51145
  
- (A) NAME: Mundy, John
- (B) STREET: NY Carlsberg Vej 6, 4th
- (C) CITY: V Copenhagen
- (E) COUNTRY: Denmark
- (F) POSTAL CODE (ZIP): 1760
  
- (A) NAME: Schell, Jeff
- (B) STREET: Carl-von-Linne-Weg 10
- (C) CITY: Koeln
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 50829
  
- (A) NAME: Eckes, Peter
- (B) STREET: Am Flachsland 18
- (C) CITY: Kelkheim (Taunus)
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 65779
  
- (A) NAME: Chet, Ilan
- (B) STREET: Shikun Ezrachi
- (C) CITY: Nes Ziona
- (E) COUNTRY: Israel
- (F) POSTAL CODE (ZIP): 70400

(ii) TITLE OF INVENTION: Transgenic pathogen-resistant organism

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Baker & Botts  
(B) STREET: 30 Rockefeller Plaza  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10112

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: reissue application of U.S. Patent No. 5,804,184  
(B) FILING DATE: herewith

(vii) ATTORNEY/AGENT INFORMATION:

(A) ATTORNEY NAME: Tenser, Arthur  
(B) REGISTRATION NUMBER: 18,839  
(C) AGENT NAME: Kole, Lisa  
(D) REGISTRATION NUMBER: 35,225  
(E) REFERENCE NO: A29542 FWC I- 37/31335

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 408-2500  
(B) TELEFAX: (212) 765-2519  
(C) TELEX: 238555

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus giganteus*

(ix) FEATURE:

(A) NAME/KEY: 5'UTR  
(B) LOCATION: 1..45

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 46..225  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION: /codon\_start= 46  
/function= "antifungal agent"

/product= "antifungal peptide)"  
 /evidence= EXPERIMENTAL  
 /note= "antifungal agent, especially on  
 Rhizoctonia solani, various Aspergillus, Fusaria  
 and Trichophyton species"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTGCCACCCC CGTTGAAGCC GATTCTCTCA CCGCTGGTGG TCTGG ATG CAA GAG	54
Met Gln Glu	
1	
ATG AGA GCG CGG GTT TTG GCC ACA TAC AAT GGC AAA TGC TAC AAG AAG	102
Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys	
5 10 15	
GAT AAT ATC TGC AAG TAC AAG GCA CAG AGC GGC AAG ACT GCC ATT TGC	150
Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys	
20 25 30 35	
AAG TGC TAT GTC AAA AAG TGC CCC CGC GAC GGC GCG AAA TGC GAG TTT	198
Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe	
40 45 50	
GAC AGC TAC AAG GGG AAG TGC TAC TGC TAGACGGTGA GCGAAGGGAC	245
Asp Ser Tyr Lys Gly Lys Cys Tyr Cys	
55 60	
GAAGTAGGCT GGGGGTTATT TTACTCTGCT	275

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gln Glu Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys	
1 5 10 15	
Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr	
20 25 30	
Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys	

35

40

45

Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys  
50 55 60

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus giganteus*

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: /note= "active protein fragment of AFP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala	Thr	Tyr	Asn	Gly	Lys	Cys	Tyr	Lys	Lys	Asp	Asn	Ile	Cys	Lys	Tyr
1				5				10					15		
Lys	Ala	Gln	Ser	Gly	Lys	Thr	Ala	Ile	Cys	Lys	Cys	Tyr	Val	Lys	Lys
			20				25						30		
Cys	Pro	Arg	Asp	Gly	Ala	Lys	Cys	Glu	Phe	Asp	Ser	Tyr	Lys	Gly	Lys
		35				40					45				
Cys	Tyr	Cys													
		50													

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hordeum vulgare*
- (B) STRAIN: L.cv. Piggy

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA gene bank in lambda-gt-11-phages

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..42

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..885
- (D) OTHER INFORMATION: /codon\_start= 43  
/function= "antifungal activity"  
/product= "protein synthesis inhibitor (PSI)"  
/note= "antifungal activity, especially on spores  
of *Trichoderma reesii* and *Fusarium sporotrichoides*  
and on *Rhizoctonia solani*."

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 886..1032
- (D) OTHER INFORMATION: /partial  
/note= "46 nucleotides at the 3'-end not shown."

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 930..935
- (D) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 963..976
- (D) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 1002..1011
- (D) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 46..886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CTTAATAGCA CATCTTGTCC GTCTTAGCTT TGCATTACAT CC ATG GCG GCA AAG